

09/5-81,106

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NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 Dec 17 The CA Lexicon available in the CAPLUS and CA files
NEWS 3 Feb 06 Engineering Information Encompass files have new names
NEWS 4 Feb 16 TOXLINE no longer being updated
NEWS 5 Apr 23 Search Derwent WPINDEX by chemical structure
NEWS 6 Apr 23 PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
NEWS 7 May 07 DGENE Reload
NEWS 8 Jun 20 Published patent applications (A1) are now in USPATFULL
NEWS 9 JUL 13 New SDI alert frequency now available in Derwent's DWPI and DPCI
NEWS 10 Aug 23 In-process records and more frequent updates now in MEDLINE
NEWS 11 Aug 23 PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
NEWS 12 Aug 23 Adis Newsletters (ADISNEWS) now available on STN
NEWS 13 Sep 17 IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH
NEWS 14 Oct 09 Korean abstracts now included in Derwent World Patents Index
NEWS 15 Oct 09 Number of Derwent World Patents Index updates increased
NEWS 16 Oct 15 Calculated properties now in the REGISTRY/ZREGISTRY File
NEWS 17 Oct 22 Over 1 million reactions added to CASREACT
NEWS 18 Oct 22 DGENE GETSIM has been improved
NEWS 19 Oct 29 AAASD no longer available
NEWS 20 Nov 19 New Search Capabilities USPATFULL and USPAT2
NEWS 21 Nov 19 TOXCENTER(SM) - new toxicology file now available on STN
NEWS 22 Nov 29 COPPERLIT now available on STN
NEWS 23 Nov 29 DWPI revisions to NTIS and US Provisional Numbers
NEWS 24 Nov 30 Files VETU and VETB to have open access
NEWS 25 Dec 10 WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
NEWS 26 Dec 10 DGENE BLAST Homology Search

NEWS EXPRESS August 15 CURRENT WINDOWS VERSION IS V6.0c,
CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP),
AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
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=> s allele specific (10a) amplif? (10a) (multiple or multiplex)
L1 57 ALLELE SPECIFIC (10A) AMPLIF? (10A) (MULTIPLE OR MULTIPLEX)

=> s l1 and polymorphism#1 and range#1
'#' TRUNCATION SYMBOL NOT VALID WITHIN 'POLYMORPHISM#1'
'#' TRUNCATION SYMBOL NOT VALID WITHIN 'POLYMORPHISM#1'
'#' TRUNCATION SYMBOL NOT VALID WITHIN 'POLYMORPHISM#1'
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to search for both 'woman' and 'women'. Enter "HELP TRUNCATION" at an
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L2 2 L1 AND POLYMORPHISM# AND RANGE#

=> s l2 and kit#
L3 0 L2 AND KIT#

=> s l2 and solid#
L4 0 L2 AND SOLID#

=> d l2 1-2 bib ab

L2 ANSWER 1 OF 2 MEDLINE
AN 2000403105 MEDLINE
DN 20387081 PubMed ID: 10926885
TI Rapid detection of the CYP2D6*3, CYP2D6*4, and CYP2D6*6 alleles by tetra-primer PCR and of the CYP2D6*5 allele by multiplex long PCR.
AU Hersberger M; Marti-Jaun J; Rentsch K; Hanseler E
CS Institute of Clinical Chemistry, University Hospital Zurich, Raemistrasse 100, CH-8091 Zurich, Switzerland.. hmr@ikc.unizh.ch
SO CLINICAL CHEMISTRY, (2000 Aug) 46 (8 Pt 1) 1072-7.
Journal code: DBZ; 9421549. ISSN: 0009-9147.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200008
ED Entered STN: 20000901
Last Updated on STN: 20000901
Entered Medline: 20000821
AB BACKGROUND: Interindividual differences in CYP2D6 activity range from total absence of metabolism of certain drugs to ultrafast metabolism and can produce adverse effects or lack of therapeutic effect under

standard therapy. Several mutations have been described in the CYP2D6 gene that abolish CYP2D6 activity. However, four mutations explain the majority of the poor metabolizers. We describe four single-tube assays to detect these mutations. METHODS: Three tetra-primer PCR assays were developed to detect the mutations in the CYP2D6*3, *4, and *6 alleles. In these single-tube assays, the CYP2D6 locus is **amplified** directly, followed by the **allele-specific amplification** on this new template. In addition, a **multiplex** long PCR was developed to genotype the CYP2D6*5 allele. Two long PCR amplifications for detection of the deletion of CYP2D6 (*5) and for detection of the CYP2D6 gene region were combined in one tube. RESULTS: Analysis of 114 alleles showed no CYP2D6*3 allele, and allele frequencies of 28.1% for CYP2D6*4, 2.6% for CYP2D6*5, and 0.9% for CYP2D6*6. Re-analysis of the DNA samples by restriction fragment length **polymorphism** and sequencing analysis confirmed these results. Furthermore, re-analysis of sequenced genomic DNA by tetra-primer PCR analysis (7-11 times) always showed identical results. CONCLUSIONS: Our set of single-tube assays allows rapid and reproducible genotyping of the majority of CYP2D6 poor metabolizers.

L2 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:396892 BIOSIS
DN PREV200000396892
TI Rapid detection of the CYP2D6*3, CYP2D6*4, and CYP2D6*6 alleles by tetra-primer PCR and of the CYP2D6*5 allele by multiplex long PCR.
AU Hersberger, Martin (1); Marti-Jaun, Jacqueline; Rentsch, Katharina; Hanseler, Edgar
CS (1) Institute of Clinical Chemistry, University Hospital Zurich,
Raemistrasse 100, CH-8091, Zurich Switzerland
SO Clinical Chemistry, (August, 2000) Vol. 46, No. 8 Part 1, pp. 1072-1077.
print.
ISSN: 0009-9147.
DT Article
LA English
SL English
AB Background: Interindividual differences in CYP2D6 activity **range** from total absence of metabolism of certain drugs to ultrafast metabolism and can produce adverse effects or lack of therapeutic effect under standard therapy. Several mutations have been described in the CYP2D6 gene that abolish CYP2D6 activity. However, four mutations explain the majority of the poor metabolizers. We describe four single-tube assays to detect these mutations. Methods: Three tetra-primer PCR assays were developed to detect the mutations in the CYP2D6*3, *4, and *6 alleles. In these single-tube assays, the CYP2D6 locus is **amplified** directly, followed by the **allele-specific amplification** on this new template. In addition, a **multiplex** long PCR was developed to genotype the CYP2D6*5 allele. Two long PCR amplifications for detection of the deletion of CYP2D6 (*5) and for detection of the CYP2D6 gene region were combined in one tube. Results: Analysis of 114 alleles showed no CYP2D6*3 allele, and allele frequencies of 28.1% for CYP2D6*4, 2.6% for CYP2D6*5, and 0.9% for CYP2D6*6. Re-analysis of the DNA samples by restriction fragment length **polymorphism** and sequencing analysis confirmed these results. Furthermore, re-analysis of sequenced genomic DNA by tetra-primer PCR analysis (7-11 times) always showed identical results. Conclusions: Our set of single-tube assays allows rapid and reproducible genotyping of the majority of CYP2D6 poor metabolizers.

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